SEQUENCE LISTING

<110> DSM N.V.
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      van LUIJK, Nicole
      JORE, Johannes
      LUITEN, Rudolf

<120> Propionibacterium Vector

<130> MBHB00-1314

<140> US 09/720,583
<141> 2000-12-22

<150> PCT/EP99/04416
<151> 1999-06-25

<150> EP 98305033.7
<151> 1998-06-25

<160> 13

<170> PatentIn version 3.0

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cgggggatgt ttggcagggg atgtggaaag agagttcgct ttgctcacat ggctcaaccg 180

ggtaactaac tgatatgggg tcttcgtcgc ccactttgaa cacgccgagg aatggaccac 240

gctgaacgtg actcgcatgc ttcactgcat gt atg gat tcg ttc gag acg ttg   293
                                  Met Asp Ser Phe Glu Thr Leu
                                  1   5

ttc cct gag agc tgg ctg cca cgc aag ccg ctg gcg tca gcc gag aag   341
Phe Pro Glu Ser Trp Leu Pro Arg Lys Pro Leu Ala Ser Ala Glu Lys
        10   15   20

tct ggg gcg tac cgg cac gtg act cgg cag agg gcg ctg gag ctg cct   389
Ser Gly Ala Tyr Arg His Val Thr Arg Gln Arg Ala Leu Glu Leu Pro
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tac atc gaa gcg aac ccg ttg gtc atg cag tcc ttg gtc atc acc gat   437

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Tyr Ile Glu Ala Asn Pro Leu Val Met Gln Ser Leu Val Ile Thr Asp
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cga gat gct tcg gat gct gac tgg gcc gca gac ctc gct ggg ctg cct    485
Arg Asp Ala Ser Asp Ala Asp Trp Ala Ala Asp Leu Ala Gly Leu Pro
                60              65              70

tca ccg tcc tac gtg tcc atg aac cgt gtc acg acc acc gga cac atc    533
Ser Pro Ser Tyr Val Ser Met Asn Arg Val Thr Thr Thr Gly His Ile
            75              80              85

gtc tat gcc ttg aag aac cct gtg tgt ctg acc gat gcc gcg cgg cga    581
Val Tyr Ala Leu Lys Asn Pro Val Cys Leu Thr Asp Ala Ala Arg Arg
        90              95              100

cgg cct atc aac ctg ctc gcc cgc gtc gag cag ggc cta tgc gac gtt    629
Arg Pro Ile Asn Leu Leu Ala Arg Val Glu Gln Gly Leu Cys Asp Val
    105             110             115

ctc ggc ggc gat gca tcc tac ggg cac cgg atc aca aag aac ccg ctc    677
Leu Gly Gly Asp Ala Ser Tyr Gly His Arg Ile Thr Lys Asn Pro Leu
120             125             130             135

agc acc gcc cat gcg acc ctc tgg ggc ccc gca gac gcg ctc tac gag    725
Ser Thr Ala His Ala Thr Leu Trp Gly Pro Ala Asp Ala Leu Tyr Glu
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ctg cgc gcc ctc gca cac acc ctc gac gag atc cac gca ctg ccg gag    773
Leu Arg Ala Leu Ala His Thr Leu Asp Glu Ile His Ala Leu Pro Glu
        155             160             165

gca ggg aac ccg cgt cgc aac gtc acc cga tca acg gtc ggc cgc aac    821
Ala Gly Asn Pro Arg Arg Asn Val Thr Arg Ser Thr Val Gly Arg Asn
            170             175             180

gtc acc ctg ttc gac acc acc cgc atg tgg gca tac cgg gcc gtc cgg    869
Val Thr Leu Phe Asp Thr Thr Arg Met Trp Ala Tyr Arg Ala Val Arg
        185             190             195

cac tcc tgg ggc ggc ccg gtc gcc gaa tgg gag cac acc gta ttc gag    917
His Ser Trp Gly Gly Pro Val Ala Glu Trp Glu His Thr Val Phe Glu
200             205             210             215

cac atc cac cta ctg aac gag acg atc atc gcc gac gaa ttc gcc aca    965
His Ile His Leu Leu Asn Glu Thr Ile Ile Ala Asp Glu Phe Ala Thr
                220             225             230

ggc ccc ctc ggc ttg aac gaa ctt aag cac tta tct cga tcc att tcc   1013
Gly Pro Leu Gly Leu Asn Glu Leu Lys His Leu Ser Arg Ser Ile Ser
            235             240             245

cga tgg gtc tgg cgc aac ttc acc ccc gaa acc ttc cgc gca cgc cag   1061
Arg Trp Val Trp Arg Asn Phe Thr Pro Glu Thr Phe Arg Ala Arg Gln
        250             255             260

aaa gcg atc agc ctc cgt gga gca tcc aaa ggc ggc aaa gaa ggc ggc   1109
Lys Ala Ile Ser Leu Arg Gly Ala Ser Lys Gly Gly Lys Glu Gly Gly
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2

cac aaa ggc ggc att gcc agt ggc gca tca cgg cgc gcc cat acc cgt   1157
His Lys Gly Gly Ile Ala Ser Gly Ala Ser Arg Arg Ala His Thr Arg
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caa cag ttc ttg gag ggt ctc tca tga ccacacgtga acgtctcccc   1204
Gln Gln Phe Leu Glu Gly Leu Ser
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Gln Arg Ala Leu Glu Leu Pro Tyr Ile Glu Ala Asn Pro Leu Val Met
        35                  40                  45

Gln Ser Leu Val Ile Thr Asp Arg Asp Ala Ser Asp Ala Asp Trp Ala
    50                  55                  60

Ala Asp Leu Ala Gly Leu Pro Ser Pro Ser Tyr Val Ser Met Asn Arg
65                  70                  75                  80

Val Thr Thr Thr Gly His Ile Val Tyr Ala Leu Lys Asn Pro Val Cys
                85                  90                  95
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4

Leu Thr Asp Ala Ala Arg Arg Arg Pro Ile Asn Leu Leu Ala Arg Val
          100   105   110

Glu Gln Gly Leu Cys Asp Val Leu Gly Gly Asp Ala Ser Tyr Gly His
          115   120   125

Arg Ile Thr Lys Asn Pro Leu Ser Thr Ala His Ala Thr Leu Trp Gly
     130   135   140

Pro Ala Asp Ala Leu Tyr Glu Leu Arg Ala Leu Ala His Thr Leu Asp
145   150   155   160

Glu Ile His Ala Leu Pro Glu Ala Gly Asn Pro Arg Arg Asn Val Thr
               165   170   175

Arg Ser Thr Val Gly Arg Asn Val Thr Leu Phe Asp Thr Thr Arg Met
          180   185   190

Trp Ala Tyr Arg Ala Val Arg His Ser Trp Gly Gly Pro Val Ala Glu
          195   200   205

Trp Glu His Thr Val Phe Glu His Ile His Leu Leu Asn Glu Thr Ile
     210   215   220

Ile Ala Asp Glu Phe Ala Thr Gly Pro Leu Gly Leu Asn Glu Leu Lys
225   230   235   240

His Leu Ser Arg Ser Ile Ser Arg Trp Val Trp Arg Asn Phe Thr Pro
               245   250   255

Glu Thr Phe Arg Ala Arg Gln Lys Ala Ile Ser Leu Arg Gly Ala Ser
          260   265   270

Lys Gly Gly Lys Glu Gly Gly His Lys Gly Gly Ile Ala Ser Gly Ala
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Ser Arg Arg Ala His Thr Arg Gln Gln Phe Leu Glu Gly Leu Ser
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Ala Ala Lys Lys Leu Gly Val Ser Glu Ser Thr Val Lys Arg Trp Thr
          20   25   30

Ser Glu Pro Arg Glu Glu Phe Val Ala Arg Val Ala Ala Arg His Ala
          35   40   45

Arg Ile Arg Glu Leu Arg Ser Glu Gly Gln Ser Met Arg Ala Ile Ala

5

Ala Glu Val Gly Val Ser Val Gly Thr Val His Tyr Ala Leu Asn Lys
 65   70   75   80

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<210> 6
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<220>
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<210> 7
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tgccgatcct ggttgc   76

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